Amendments to the Specification:

Please substitute paragraphs [0090], [0091] and [0096] with the following amended replacement paragraphs [0090], [0091] and [0096].

[0090] However, alanine scanning of the starting peptide ($mEGF_{(33-42)}$) indicated that residues at positions 1, 2, 3, and 6 (peptides VI, VII, VIII and X respectively) (SEQ ID NO: 21, 22, 23 AND 25 respectively), are essential for receptor mediated activities as determined by ^{125}I-laminin displacement and cell attachment to laminin through the 67-LR. Substitution of these individual residues by alanine leads to a dramatic decrease in receptor affinity observed as an increased IC_{50} (~~Table 2~~ Table 1b) and a parallel decrease in their ability to block adhesion to laminin (increased EC_{50}; ~~Table 2~~ Table 1b). Characterisation of these analogues with regard to effects on motility, largely confirmed these findings although there was one exception; peptide VIII (SEQ ID NO: 23). Results from the migration assay identified this sequence (alanine for cysteine (P1)) as being a weak laminin agonist despite there being a much reduced response in the other two assays. It is suggested that this peptide may influence laminin receptor mediated migration through an alternative mechanism (Scott 1997).

[0091] Substitution at P10 (alanine for cysteine ~~(peptide X) (SEQ ID NO: 25)~~ (peptide IX) (SEQ ID NO:24)) retains both receptor binding and adhesion displacing activities but has the effect of changing the antagonistic parent into an agonist analogue. This reflects the response the agonism of Lam.β-$1_{(925-933)}$, which also lacks the *C*-terminal cysteine, and suggests that this cysteine is not essential for receptor recognition, but is required for antagonism of $mEGF_{(33-42)}$.

[0096] It was found that replacement of arginine (P9) with citrulline (peptide IV) (SEQ ID NO: 19) increased both receptor binding and inhibition of attachment to laminin substrata whilst retaining antagonist migratory response (~~Table 2~~ Table 1a), reinforcing the observation that it is not the positive charge that is required rather than an active conformation generated by hydrogen bonding. These findings thus identify H-bonding between P5 and P9 as being more important than the charge at the P9 arginine in determining antagonist activity. Subsequent strategies involved the substitution of variant residues in the antagonistic $mEGF_{(33-42)}$ with those present in the agonistic Lam.β-$1_{(925-933)}$ sequence (peptides I-III) (SEQ ID NO: 16, 17 AND 18), in an effort to identify key amino acids in the *C*-terminal regions (P5-10) of the two ligands responsible for their contrasting bioactivities.